#### **EAST Search History**

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	13	((magnesium with (deficit or deficiency or reduce or reduced or diminish or diminished or lower or decrease or decreased)) with (hypertension or diabetes)) and ((magnesium with (deficit or deficiency or reduce or reduced or diminish or diminished or lower or decrease or decreased)) with (preeclampsia or eclampsia or (pre 2adj eclampsia)))	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/08/11 08:35
L2	1037902	preeclampsia or eclampsia or (pre 2adj eclampsia)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/08/11 08:35
L3	346845	(substance adj P) or SP or tachykinin or neurokinin or NKA or NKB	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/08/11 08:35
L4	4769774	assay or test or elisa or quantitate or quantify or detect or detection or determine or determination	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/08/11 08:35
L5	88623	L4 with L2	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/08/11 08:35
L6	166	L5 with L3	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/08/11 08:35
L7	59	L6 and magnesium	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/08/11 08:35
L8	12	(wells and ibert).in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/08/11 08:36

Page 1

### SCORE Search Results Details for Application 10805881 and Search Result us-10-805-881. 1.max.rai.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10805881 and Search Result us-10-80 1.max.rai.

start

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 17:41:48; Search time 21 Seconds

(without alignments)

20.841 Million cell updates/sec

Title: US-10-805-881-1

Perfect score: 27

Sequence: 1 FFGLM 5

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 31763

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:\* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:\* 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\* 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\* 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*

6: /EMC Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\* 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No. Score Match Length DB ID Description

http://es/ScoreAccessWeb/GetItem.action?AppId=10805881&seqId=581914&ItemName=us... 8/11/06

Issued Patents AA:\*

-			_	_	03 004 550 0	_	
1	27	100.0	5	1	US-07-934-553-2		2, Appli
2	27	100.0	5	1	US-08-225-474-2		2, Appli
3	27	100.0	5	1	US-07-737-371E-6	Sequence	6, Appli
4	27	100.0	5	2	US-09-265-690C-1	Sequence	1, Appli
5	27	100.0	5	2	US-09-623-548A-604	Sequence	604, App
6	27	100.0	5	2	US-10-134-187-3		3, Appli
7	27	100.0	5	2	US-09-657-276-604	_	604, App
8	24	88.9	5	1	US-07-737-371E-48		48, Appl
9	22	81.5	5	1	US-07-737-371E-47		47, Appl
10	22	81.5	5	1	US-07-737-371E-49		49, Appl
11	21	77.8	4	1	US-08-441-591-63	_	
12		77.8	_			-	63, Appl
	21		4	1	US-08-303-362A-63		63, Appl
13	21	77.8	4	2	US-09-265-690C-2	_	2, Appli
14	21	77.8	4	2	US-09-635-266-3		3, Appli
15	21	77.8	4	2	US-10-230-133-3		3, Appli
16	21	77.8	4	2	US-09-623-548A-623	Sequence	623, App
17	21	77.8	4	2	US-10-695-536-3	Sequence	3, Appli
18	21	77.8	4	2	US-09-657-276-623	Sequence	623, App
19	21	77.8	4	5	PCT-US95-05600-80	_	80, Appl
20	21	77.8	5	1	US-08-070-301-6	<del>-</del>	6, Appli
21	21	77.8	5	2	US-09-623-548A-565		565, App
22	21	77.8	5	2	US-09-657-276-565		565, App
23	20	74.1	5	1	US-07-753-909B-3		
							3, Appli
24	20	74.1	5	1	US-08-269-288-1	_	1, Appli
25	20	74.1	5	1	US-08-391-910-1	<del>-</del>	1, Appli
26	20	74.1	5	1	US-08-418-994-1		1, Appli
27	20	74.1	5	1	US-08-391-814-1		1, Appli
28	20	74.1	5	1	US-08-441-591-61	Sequence	61, Appl
29	20	74.1	5	1	US-08-303-362A-61	Sequence	61, Appl
30	. 20	74.1	5	1	US-08-462-415-1	Sequence	1, Appli
31	20	74.1	5	1	US-08-463-874-1	_	1, Appli
32	20	74.1	5	1	US-08-444-135-1	_	1, Appli
33	20	74.1	5	1	US-08-318-391-1		1, Appli
34	20	74.1	5	2	US-08-257-966-1		1, Appli
35	20	74.1	5	2	US-09-265-690C-4		4, Appli
36	20	74.1	5	2	US-08-153-847-1		1, Appli
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						_	4, Appli
38	20	74.1	5	2	US-10-230-133-4	_	4, Appli
39	20	74.1	5	2	US-10-695-536-4	<del>-</del>	4, Appli
40	20	74.1	5	2	US-10-668-565-1		1, Appli
41	20	74.1	<sub>.</sub> 5	5	PCT-US95-05600-78	Sequence	78, Appl
42	19	70.4	4	2	US-08-722-126A-20	Sequence	20, Appl
43	19	70.4	5	1	US-08-765-061-5	Sequence	5, Appli
44	19	70.4	5	2	US-09-623-548A-606	Sequence	606, App
45	19	70.4	5	2	US-09-657-276-606	Sequence	606, App
46	18	66.7	3	2	US-09-623-548A-1527		1527, Ap
47	18	66.7	3	2	US-09-657-276-1527		1527, Ap
48	18	66.7	4	1	US-07-822-924-7		7, Appli
49	18	66.7	4	ī	US-08-285-777-1		1, Appli
50	18	66.7	4	1	US-08-127-904-11		11, Appl
					US-08-431-539-4		
51 52	18	66.7	4	1			4, Appli
52	18	66.7	4	1	US-09-060-455-16		16, Appl
53	18	66.7	4	2	US-09-082-279B-826		826, App
54	18	66.7	4	2	US-09-264-709A-12		12, Appl
55	18	66.7	4	2	US-09-264-709A-18		18, Appl
56	18	66.7	4	2	US-09-264-709A-19		19, Appl
57	18	66.7	4	2	US-09-264-709A-23		23, Appl
58	18	66.7	4	2	US-09-264-709A-24	Sequence	24, Appl
59	18	66.7	4	2	US-09-264-709A-34		34, Appl
60	18	66.7	4	2	US-09-315-304B-826	_	826, App
61	18	66.7	4	2	US-09-147-342B-4		4, Appli
						•	

# SCORE Search Results Details for Application 10805881 and Search Result us-10-805-881 1.max.rapbm.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10805881 and Search Result us-10-80 1.max.rapbm.

start

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

August 10, 2006, 17:57:39 ; Search time 119.5 Seconds Run on:

(without alignments)

19.381 Million cell updates/sec

Title: US-10-805-881-1

Perfect score: 27

Sequence: 1 FFGLM 5

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 37972

Minimum DB seg length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\* 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\* 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		% Ouerv				
No.	Score	~ 2	Length	DB	ID	Description
1	<b></b> 27	100.0	5	<b>-</b> -	US-09-265-690C-1	Sequence 1, Appli

2	27	100.0	5	4	US-10-053-669-1	Company 1 Danie
2	27			-		Sequence 1, Appli
3	27	100.0	5	4	US-10-134-187-3	Sequence 3, Appli
4	27	100.0	5	4	US-10-688-741-3	Sequence 3, Appli
5	27	100.0	5	4	US-10-805-881-1	Sequence 1, Appli
6	27	100.0	5	5	US-10-720-039-3	Sequence 3, Appli
7	27	100.0	5	5	US-10-497-628-15	Sequence 15, Appl
8	27	100.0	5	6	US-11-066-697-604	Sequence 604, App
9	27	100.0	5	6	US-11-025-494-3	Sequence 3, Appli
10	27	100.0	5	6	US-11-041-270A-12	Sequence 12, Appl
11	24	88.9	5	5	US-10-497-628-16	Sequence 16, Appl
12	22	81.5	4	5	US-10-821-240A-270	Sequence 270, App
13	21	77.8	4	3	US-09-265-690C-2	Sequence 2, Appli
14	21	77.8	4	4	US-10-230-133-3	Sequence 3, Appli
15	21	77.8	4	4	US-10-053-669-2	Sequence 2, Appli
16	21	77.8	4	4	US-10-695-536-3	Sequence 3, Appli
17	21	77.8	4	4	US-10-805-881-2	Sequence 2, Appli
18	21	77.8	4	5	US-10-497-628-2	Sequence 2, Appli
19	21	77.8	4	6	US-11-018-690-3	Sequence 3, Appli
20	21	77.8	4	6	US-11-066-697-623	Sequence 623, App
21	21	77.8	4	6	US-11-041-270A-13	Sequence 13, Appl
22	21	77.8	4	6	US-11-292-460-3	Sequence 3, Appli
23	21	77.8	5	4	US-10-346-737A-30	
24	21	77.8		-		Sequence 30, Appl
			5	5	US-10-497-628-17	Sequence 17, Appl
25	21	77.8	5	6	US-11-066-697-565	Sequence 565, App
26	20	74.1	5	3	US-09-265-690C-4	Sequence 4, Appli
27	20	74.1	5	4	US-10-230-133-4	Sequence 4, Appli
28	20	74.1	5	4	US-10-053-669-4	Sequence 4, Appli
29	20	74.1	5	4	US-10-695-536-4	Sequence 4, Appli
30	20	74.1	5	4	US-10-805-881-4	Sequence 4, Appli
31	20	74.1	5	5	US-10-451-304-12	Sequence 12, Appl
32	20	74.1	5	6	US-11-018-690-4	Sequence 4, Appli
33	20	74.1	5	6	US-11-292-460-4	Sequence 4, Appli
34	19	70.4	5	4	US-10-346-737A-22	Sequence 22, Appl
35	19	70.4	. 5	6	US-11-066-697-606	Sequence 606, App
36	18	66.7	3	6	US-11-066-697-1527	Sequence 1527, Ap
37	18	66.7	3	6	US-11-106-623-27	Sequence 27, Appl
3,8	18	66.7	4	2	US-08-484-409-14	Sequence 14, Appl
39	18	66.7	4	4	US-10-155-170-4	Sequence 4, Appli
40	18	66.7	4	4	US-10-351-641-826	Sequence 826, App
41	18	66.7	4	4	US-10-822-661-4	Sequence 4, Appli
42	18	66.7	4	5	US-10-821-240A-298	Sequence 298, App
43	18	66.7	4	5	US-10-878-175B-3	Sequence 3, Appli
44	18	66.7	4	5	US-10-467-657-8994	Sequence 8994, Ap
45	18	66.7	4	5	US-10-895-064-192	Sequence 192, App
46	18	66.7	4	5	US-10-923-112A-3	Sequence 3, Appli
47	18	66.7	4	6	US-11-129-741-192	Sequence 192, App
48	18	66.7	4	6	US-11-129-741-3125	Sequence 3125, Ap
49	18	66.7	5	3	US-09-920-306-38	Sequence 38, Appl
50	17	63.0	5	4	US-10-168-789A-32	Sequence 32, Appl
51	17	63.0	5	5	US-10-783-311-299	Sequence 299, App
52	16	59.3	4	3	US-09-879-442A-9	Sequence 9, Appli
53	16	59.3	5	3	US-09-886-135-2	Sequence 2, Appli
54	16	59.3	5	4	US-10-620-052A-45	Sequence 45, Appli
55	16	59.3	5	4	US-10-337-105-3	Sequence 3, Appli
56	16	59.3	5	4	US-10-337-105-3 US-10-337-105-4	Sequence 4, Appli
56 57	16	59.3	5	5	US-10-337-105-4 US-10-891-122-2	
5 <i>1</i>			5 5	5		Sequence 2, Appli
58 59	16 16	59.3	5 5	5 5	US-10-894-672-94	Sequence 94, Appl
		59.3			US-10-996-316-94	Sequence 94, Appl
60	16	59.3	5 5	5	US-10-975-323-29	Sequence 29, Appl
61 62	16 15	59.3	3	6	US-11-171-567-94	Sequence 94, Appl
02	15	55.6	3	4	US-10-230-133-2	Sequence 2, Appli

## **SCORE Search Results Details for Application** 10805881 and Search Result us-10-805-881-1.max.rapbn.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10805881 and Search Result us-10-80 1.max.rapbn.

start

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```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

August 10, 2006, 17:58:09; Search time 20 Seconds Run on:

(without alignments)

16.828 Million cell updates/sec

Title: US-10-805-881-1

Perfect score: 27

Sequence: 1 FFGLM 5

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 239914 segs, 67312017 residues

Total number of hits satisfying chosen parameters: 2632

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:\*

> 1: /EMC Celerra SIDS3/ptodata/1/pubpaa/US09 NEW PUB.pep:\* 2: /EMC Celerra SIDS3/ptodata/1/pubpaa/US06 NEW PUB.pep:\*

> 3: /EMC Celerra SIDS3/ptodata/1/pubpaa/US07 NEW PUB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

/EMC Celerra SIDS3/ptodata/1/pubpaa/US10 NEW\_PUB.pep:\* /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

/EMC Celerra SIDS3/ptodata/1/pubpaa/US60 NEW PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

용

Score Match Length DB ID Description

1	14	51.9	4	6	US-10-342-232-25	Sequence 25, Appl
2	14	51.9	5	6	US-10-972-962-127	Sequence 127, App
3	14	51.9	5	7	US-11-111-688-19	Sequence 19, Appl
4	13	48.1	4	6	US-10-524-434-500	Sequence 500, App
5	13	48.1	5	7	US-11-298-344-64	Sequence 64, Appl
6	12	44.4	4	6	US-10-828-623C-3	Sequence 3, Appli
7	12	44.4	4	6	US-10-524-434-195	Sequence 195, App
8	12	44.4	4	6	US-10-524-434-196	Sequence 196, App
9	12	44.4	4	. 6	US-10-524-434-197	Sequence 197, App
10	12	44.4	4	6	US-10-524-434-369	Sequence 369, App
11	12	44.4	4	6	US-10-524-434-370	Sequence 370, App
12	12	44.4	4	6	US-10-524-434-502	Sequence 502, App
13	12	44.4	4	7	US-11-252-276-86	Sequence 86, Appl
14	12	44.4	4	7	US-11-251-734-13	Sequence 13, Appl
15	12	44.4	4	7	US-11-303-372-113	Sequence 113, App
16	12	44.4	4	7	US-11-303-372-119	Sequence 119, App
17	12	44.4	4	7	US-11-178-538-67	Sequence 67, Appl
18	12	44.4	4	7	US-11-199-062-90	Sequence 90, Appl
19	12	44.4	4	7	US-11-300-194-50	Sequence 50, Appl
20	12	44.4	4	7	US-11-036-257-105	Sequence 105, App
21	12	44.4	4	7	US-11-366-462-13	Sequence 13, Appl
22	12	44.4	4	7	US-11-240-962-61	Sequence 61, Appl
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24	12	44.4	5	6	US-10-520-386-2	Sequence 2, Appli
25	12	44.4	5	6	US-10-520-386-3	Sequence 3, Appli
26	12	44.4	5	6	US-10-510-809-1	Sequence 1, Appli
27	12	44.4	5	6	US-10-510-809-4	Sequence 4, Appli
28	12	44.4	5	6	US-10-510-809-5	Sequence 5, Appli
29	12	44.4	5	6	US-10-561-015-8	Sequence 8, Appli
30	12	44.4	5	6	US-10-518-884-16	Sequence 16, Appl
31	12	44.4	5	6	US-10-546-901-12	Sequence 12, Appl
32	12	44.4	5	7	US-11-298-344-17	Sequence 17, Appl
33	12	44.4	5	7	US-11-298-344-62	Sequence 62, Appl
34	12	44.4	5	7	US-11-298-344-90	Sequence 90, Appl
35	12	44.4	5	7	US-11-269-857-7	Sequence 7, Appli
36	12	44.4	5	7	US-11-200-907-3	Sequence 3, Appli
37	12	44.4	5	7	US-11-139-770A-6	Sequence 6, Appli
38	12	44.4	5	7	US-11-139-770A-7	Sequence 7, Appli
39	12	44.4	5	7	US-11-287-157A-25	Sequence 25, Appl
40	12	44.4	5	7	US-11-287-157A-35	Sequence 35, Appl
41	12	44.4	5	7	US-11-351-712-16	Sequence 16, Appl
42	11	40.7	4	6	US-10-524-434-499	Sequence 499, App
43	11	40.7	4	. 6	US-10-524-434-549	Sequence 549, App
44	11	40.7	4	6	US-10-524-434-550	Sequence 550, App
45	11	40.7	4	7	US-11-350-336-2	Sequence 2, Appli
46	11	40.7	5	6	US-10-497-088-8	Sequence 8, Appli
47	11	40.7	5	6	US-10-499-266-5	Sequence 5, Appli
48	11	40.7	5	6	US-10-828-623C-9	Sequence 9, Appli
49	11	40.7	5	6	US-10-521-109-8	Sequence 8, Appli
50	11	40.7	5	6	US-10-523-295-4	Sequence 4, Appli
51	11	40.7	5	7	US-11-298-344-16	Sequence 16, Appl
52	11	40.7	5	7	US-11-246-006-86	Sequence 86, Appl
53	11	40.7	5	7	US-11-246-006-87	Sequence 87, Appl
54	11	40.7	5	7	US-11-303-372-116	Sequence 116, App
55	11	40.7	5	7	US-11-023-959A-34	Sequence 34, Appl
56	11	40.7	5	7	US-11-376-338-9	Sequence 9, Appli
57	11	40.7	5	7	US-11-287-157A-16	Sequence 16, Appl
58	10	37.0	3	6	US-10-489-071-111	Sequence 111, App
59	10	37.0	3	6	US-10-489-071-117	Sequence 117, App
60	10	37.0	3	7	US-11-244-349B-7	Sequence 7, Appli
		- , • •	•	•		

### **SCORE Search Results Details for Application** 10805881 and Search Result us-10-805-881 2.max.rai.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10805881 and Search Result us-10-80 2.max.rai.

start

Go Back to pre

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

August 10, 2006, 18:02:30 ; Search time 50 Seconds Run on: (without alignments)

7.002 Million cell updates/sec

Title: US-10-805-881-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 14308

Minimum DB seq length: 0 Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:\*

> 1: /EMC\_Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:\* 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\* 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\* 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\* 5: /EMC Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\* 6: /EMC Celerra SIDS3/ptodata/2/iaa/RE\_COMB.pep:\* 7: /EMC\_Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

Score Match Length DB ID Description

•	0.1	100 0			00 441 501 60	_	
1	21	100.0	4	1	US-08-441-591-63		63, Appl
2	21	100.0	4	1	US-08-303-362A-63	Sequence	63, Appl
3	21	100.0	4	2	US-09-265-690C-2	Sequence	2, Appli
4	21	100.0	4	2	US-09-635-266-3	Sequence	3, Appli
5	21	100.0	4	2	US-10-230-133-3		3, Appli
6	21	100.0	4	2	US-09-623-548A-623	_	623, App
7	21	100.0	4	2	US-10-695-536-3	<u>-</u>	
8	21		4	2			3, Appli
		100.0			US-09-657-276-623		623, App
9	21	100.0	4	5	PCT-US95-05600-80		80, Appl
10	16	76.2	4	1	US-08-747-137-124	Sequence	124, App
11	16	76.2	4	2	US-08-722-126A-20	Sequence	20, Appl
12	15	71.4	3	2	US-09-635-266-2	Sequence	2, Appli
13	15	71.4	3	2	US-10-230-133-2	_	2, Appli
14	15	71.4	3	2	US-09-623-548A-624		624, App
15	15	71.4	3	2	US-10-695-536-2		2, Appli
16	. 15	71.4	3	2	US-09-657-276-624	<del>-</del>	
							624, App
17	15	71.4	4	1	US-08-070-301-8		8, Appli
18	15	71.4	4	1	US-08-433-401-4	Sequence	4, Appli
19	15	71.4	4	2	US-09-623-548A-971	Sequence	971, App
20	15	71.4	4	2	US-09-623-548A-998	Sequence	998, App
21	15	71.4	4	2	US-09-657-276-971		971, App
22	15	71.4	4	2	US-09-657-276-998		998, App
23	14	66.7	4	2	US-08-793-701-25		
24	14			2			25, Appl
		66.7	4		US-09-579-264-25		25, Appl
25	14	66.7	4	2	US-09-623-548A-890		890, App
26	14	66.7	4	2	US-09-657-276-890		890, App
27	13	61.9	4	1	US-08-429-964-37	Sequence	37, Appl
28	13	61.9	4	2	US-08-812-586-60	Sequence	60, Appl
29	13	61.9	4	2	US-08-669-656A-11	Sequence	
30	13	61.9	4	2	US-09-535-832A-56		56, Appl
31	13	61.9	4	2	US-09-665-362A-31	Sequence	
32	13	61.9	4	2	US-09-665-637-31	_	
						Sequence	
33	13	61.9	4	2	US-10-087-402-10		10, Appl
34	13	61.9	4	2	US-10-083-894-31	_	31, Appl
35	13,	61.9	4	2	US-10-196-394-98		98, Appl
36	13	61.9	4	5	PCT-US93-08062-37	Sequence	37, Appl
37	12	57.1	3	1	US-08-343-943-4	Sequence	4, Appli
38	12	57.1	3	1	US-09-060-455-2	Sequence	2, Appli
39	12	57.1	3	2	US-09-150-621-3		3, Appli
40	12	57.1	3	2	US-10-121-857-6		6, Appli
41	12	57.1	3	2	US-09-623-548A-1527	=	
42	12					_	1527, Ap
		57.1	3	2	US-09-657-276-1527		1527, Ap
43	12	57.1	3	2	US-10-104-307-3		3, Appli
44	12	57.1	3	2	US-10-045-545A-12		12, Appl
45	12	57.1	4	1	US-07-657-769B-58	Sequence	58, Appl
46	12	57.1	4	1	US-07-822-924-3	Sequence	3, Appli
47	12	57.1	4	1	US-07-822-924-5		5, Appli
48	12	57.1	4	1	US-07-822-924-7		7, Appli
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50	12	57.1	4	1	US-08-147-270A-1	Sequence	
51	12	57.1		1			
			4		US-07-969-307A-1	Sequence	
52	12	57.1	4	1	US-07-969-307A-2		2, Appli
53	12	57.1	4	1	US-07-969-307A-3	Sequence	
54	12	57.1	4	1	US-08-127-904-11		11, Appl
55	12	57.1	4	1	US-08-431-539-4	Sequence	4, Appli
56	12	57.1	4	1	US-08-331-383-10	Sequence	
57	12	57.1	4	1	US-08-429-732-20		20, Appl
58	12	57.1	4	1	US-07-789-184-108	Sequence	
59	12	57.1	4	1	US-08-549-008-10	_	100, Appl
60	12	57.1	4	1	US-08-624-123-11		
							11, Appl
61	12	57.1	4	1	US-08-077-252B-20	Sequence	ZU, APPI

# **SCORE Search Results Details for Application** 10805881 and Search Result us-10-805-881 2.max.rapbm.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10805881 and Search Result us-10-80 2.max.rapbm.

start

Go Back to pro

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

August 10, 2006, 18:14:00; Search time 179 Seconds Run on:

(without alignments)

10.351 Million cell updates/sec

Title: US-10-805-881-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 16442

Minimum DB seq length: 0 Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:\*

> 1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:\* 2: /EMC Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		% Querv				
No.	Score		Length	DB	ID	Description
1	21	100.0	4	<b>-</b> 3	US-09-265-690C-2	Seguence 2, Appli

^					10 000 100 0	_	
2	21	100.0	4	4	US-10-230-133-3	Sequence	
3	21	100.0	4	4	US-10-053-669-2	Sequence	2, Appli
4	21	100.0	4	4	US-10-695-536-3	Sequence	3, Appli
5	21	100.0	4	4	US-10-805-881-2	Sequence	2, Appli
6	21	100.0	4	5	US-10-497-628-2	Sequence	
7	21	100.0	4	6	US-11-018-690-3	Sequence	
8	21	100.0	4	6	US-11-066-697-623	<del>-</del>	
9						Sequence	
	21	100.0	4	6	US-11-041-270A-13	Sequence	
10	21	100.0	4	6	US-11-292-460-3	Sequence	
11	16	76.2	4	3	US-09-879-442A-9	Sequence	9, Appli
12	16	76.2	4	5	US-10-821-240A-270	Sequence	270, App
13	15	71.4	3	4	US-10-230-133-2	Sequence	
14	15	71.4	3	4	US-10-695-536-2	Sequence	
15	15	71.4	3	6	US-11-018-690-2	Sequence	
16	15	71.4	3	6	US-11-066-697-624		
						Sequence	
17	15	71.4	3	6	US-11-041-270A-14	Sequence	
18	15	71.4	3	6	US-11-292-460-2	Sequence	
19	15	71.4	4	6	US-11-066-697-971	Sequence	971, App
20	15	71.4	4	6	US-11-066-697-998	Sequence	998, App
21	14	66.7	4	3	US-09-879-442A-8	Sequence	8, Appli
22	14	66.7	4	4	US-10-137-867-328	Sequence	
23	14	66.7	4	5	US-10-433-709-17		
						Sequence	
24	14	66.7	4	6	US-11-066-697-890	Sequence	
25	13	61.9	4	3	US-09-879-442A-98	Sequence	
26	13	61.9	4	3	US-09-879-442A-99	Sequence	99, Appl
27	13	61.9	4	3	US-09-943-123-24	Sequence	24, Appl
28	13	61.9	4	4	US-10-087-905-30	Sequence	30, Appl
29	. 13	61.9	4	4	US-10-087-942-30	Sequence	
30	13	61.9	4	4	US-10-087-402-10	Sequence	-
31	13	61.9	4	4	US-10-083-894-31	_	
						Sequence	
32	13	61.9	4	4	US-10-196-394-98	Sequence	
33	13	61.9	4	4	US-10-202-824-11	Sequence	
34	13	61.9	4	4	US-10-359-363A-104	Sequence	104, App
35	13	61.9	4	5	US-10-491-418-21	Sequence	21, Appl
36	13	61.9	4	5	US-10-712-359A-24	Sequence	24, Appl
37	13	61.9	4	5	US-10-476-861A-11	Sequence	
38	13	61.9	4	5	US-10-476-861A-118	Sequence	
39	13	61.9	4	6	US-11-136-464-11	Sequence	
40	13	61.9	4	6	US-11-129-741-3978	Sequence	
41	12	57.1	3	4			
				-	US-10-121-857-6	Sequence	
42	12	57.1	3	4	US-10-255-679-3	Sequence	
43	12	57.1	3	4	US-10-208-018-6	Sequence	6, Appli
44	12	57.1	3	4	US-10-104-307-3	Sequence	3, Appli
45	12	57.1	3	6	US-11-066-697-1527	Sequence	1527, Ap
46	12	57.1	3	6	US-11-106-623-27	Sequence	
47	12	57.1	3	6	US-11-205-562-12	Sequence	
48	12	57.1	3	6	US-11-204-187-12	Sequence	
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50	12	57.1	4	2	US-08-484-409-25	Sequence	
51	12	57.1	4	3	US-09-804-733A-24	Sequence	
52	12	57.1	4	3	US-09-803-126-20	Sequence	20, Appl
53	12	57.1	4	3	US-09-726-470A-29	Sequence	29, Appl
54	12	57.1	4	3	US-09-563-222-1	Sequence	1, Appli
55	12	57.1	4	3	US-09-811-945-15	Sequence	
56	12	57.1	4	4	US-10-007-761-62	Sequence	
57	12	57.1	4	4	US-10-044-034-1	Sequence	
58	12	57.1	4	4			
					US-10-044-034-25	Sequence	
59	12	57.1	4	4	US-10-076-421-3	Sequence	
60	12	57.1	4	4	US-10-087-905-14	Sequence	
61	12	57.1	4	4	US-10-087-905-17	Sequence	
62	12	57.1	4	4	US-10-255-679-2	Sequence	2, Appli

# **SCORE Search Results Details for Application** 10805881 and Search Result us-10-805-881-2.max.rapbn.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10805881 and Search Result us-10-80 2.max.rapbn.

start

Go Back to prev

```
GenCore version 5.1.9
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```

OM protein - protein search, using sw model

August 10, 2006, 18:14:25; Search time 31 Seconds Run on: (without alignments)

8.685 Million cell updates/sec

US-10-805-881-2 Title:

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 239914 segs, 67312017 residues

Total number of hits satisfying chosen parameters: 1697

Minimum DB seq length: 0 Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:\*

> 1: /EMC Celerra SIDS3/ptodata/1/pubpaa/US09 NEW PUB.pep:\* 2: /EMC Celerra SIDS3/ptodata/1/pubpaa/US06 NEW PUB.pep:\* 3: /EMC Celerra SIDS3/ptodata/1/pubpaa/US07 NEW PUB.pep:\* 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\* 5: /EMC Celerra SIDS3/ptodata/1/pubpaa/PCT NEW PUB.pep:\* 6: /EMC Celerra SIDS3/ptodata/1/pubpaa/US10 NEW PUB.pep:\*

> 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용 Result Query

Score Match Length DB ID

Description

	1 1	L 4	66.7	4	6	US-10-342-232-25	Sequence	25, Appl
		13	61.9	4	6	US-10-524-434-500		500, App
		12	57.1	4	6	US-10-524-434-502		502, App
		12	57.1	4	7	US-11-252-276-86		86, Appl
		12	57.1	4	7	US-11-303-372-119		119, App
		12	57.1	4	7	US-11-178-538-67	-	67, Appl
		12	57.1	4	7	US-11-240-962-61	_	
		11	52.4	4	6	US-10-524-434-499		61, Appl
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			52.4	_		US-10-524-434-550		550, App
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		10	47.6	3	6	US-10-489-071-117		117, App
		10	47.6	3	7	US-11-244-349B-7		7, Appli
		10	47.6	4	6	US-10-520-386-4		4, Appli
		10	47.6	4	6	US-10-520-386-8		8, Appli
		LO	47.6	4	6	US-10-821-930-29		29, Appl
		LO	47.6	4	6	US-10-608-886A-3		3, Appli
		LO	47.6	4	6	US-10-608-886A-18		18, Appl
		LO	47.6	4	6	US-10-608-886A-20		20, Appl
		LO	47.6	4	6	US-10-608-886A-22		22, Appl
		LO	47.6	4	6	US-10-518-941-22		22, Appl
		LO	47.6	4	6	US-10-524-434-176		176, App
		LO	47.6	4	6	US-10-524-434-177		177, App
		LO	47.6	4	6	US-10-524-434-178	Sequence	178, App
		LO	47.6	4	6	US-10-524-434-185	Sequence	185, App
		LO	47.6	4	6	US-10-524-434-186	Sequence	186, App
2	7 1	L <b>O</b>	47.6	4	6	US-10-524-434-352	Sequence	352, App
2	8 1	10	47.6	4	6	US-10-524-434-353	Sequence	353, App
2	9 1	LO	47.6	4	6	US-10-524-434-354	Sequence	354, App
3	0 1	LO	47.6	4	6	US-10-524-434-548	Sequence	548, App
3	1 1	LO	47.6	4	6	US-10-524-434-564	Sequence	564, App
3	2 1	LO,	47.6	4	6	US-10-524-434-565		565, App
3	3 1	L <b>O</b>	47.6	4	6	US-10-524-434-566		566, App
3	4 1	0	47.6	4	7	US-11-181-115-67		67, Appl
3	5 1	.0	47.6	4	7	US-11-298-344-11		11, Appl
3	6 1	.0	47.6	4	7	US-11-298-344-13	Sequence	13, Appl
3	7 1	.0	47.6	4	7	US-11-335-474-8		8, Appli
3	8 1	.0	47.6	4	7	US-11-199-062-55		55, Appl
3	9 1	.0	47.6	4	7	US-11-199-062-82		82, Appl
4	0 1	.0	47.6	4	7	US-11-271-285-48	-	48, Appl
4	1 1	.0	47.6	4	7	US-11-317-806-34		34, Appl
4	2 1	.0	47.6	4	7	US-11-370-290-7		7, Appli
4	3 1	.0	47.6	4	7	US-11-335-891-124		124, App
4	4 1	.0	47.6	4	7	US-11-386-736-30		30, Appl
		.0	47.6	4	7	US-11-368-804-53		53, Appl
	6	9	42.9	4	6	US-10-524-434-83		83, Appl
4	7	9	42.9	4	6	US-10-524-434-84		84, Appl
4	8	9	42.9	4	6	US-10-524-434-85		85, Appl
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	1	9	42.9	4	6	US-10-524-434-209		209, App
	2	9	42.9	4	6	US-10-524-434-210		210, App
	3	9	42.9	4	7	US-11-303-372-118		118, App
	4	9	42.9	4	7	US-11-178-538-66		66, Appl
	5	9	42.9	4	7	US-11-253-176-131		131, App
	6	9	42.9	4	7	US-11-300-194-19		19, Appl
	7 .	9	42.9	4	7	US-11-335-891-114		114, App
	8	9	42.9	4	7	US-11-335-891-140		140, App
	9	9	42.9	4	7	US-11-335-891-197		197, App
	0	9	42.9	4	7	US-11-368-804-54		54, Appl
,	-	-		•	•			,pp+

### **SCORE Search Results Details for Application** 10805881 and Search Result us-10-805-881 4.max.rai.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10805881 and Search Result us-10-8( 4.max.rai.

<u>start</u>

Go Back to pre

```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

August 10, 2006, 17:41:48 ; Search time 21 Seconds Run on:

(without alignments)

20.841 Million cell updates/sec

US-10-805-881-4 Title:

Perfect score: 21

Sequence: 1 FXGLM 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 31763

Minimum DB seq length: 0 Maximum DB seg length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:\*

> 1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:\* 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\* 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\* 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\* 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\* 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\* 7: /EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No. Score Match Length DB ID Description

http://es/ScoreAccessWeb/GetItem.action?AppId=10805881&seqId=581924&ItemName=us... 8/11/06

-		05.0	_		07 750 0000 0	_	
1	20	95.2		1	US-07-753-909B-3		3, Appli
2	20	95.2	5 3	1	US-07-934-553-2	Sequence	2, Appli
3	20	95.2	5 :	1	US-08-269-288-1	Sequence	1, Appli
4	20	95.2	5 3	1	US-08-225-474-2	-	2, Appli
5	20	95.2		1	US-08-391-910-1		
						_	1, Appli
6	20	95.2		1	US-08-418-994-1	Sequence	1, Appli
7	20	95.2	5 :	1	US-08-391-814-1	Sequence	1, Appli
8	20	95.2	5 :	1	US-08-441-591-61	Sequence	61, Appl
9	20	95.2		1	US-08-303-362A-61	_	61, Appl
10	20	95.2		1	US-08-462-415-1		
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12	20	95.2	5 1	1	US-08-444-135-1	Sequence	1, Appli
13	20	95.2	5 :	1	US-08-318-391-1	Sequence	1, Appli
14	20	95.2	5 3	1	US-07-737-371E-6	_	6, Appli
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16	20	95.2		2	US-09-265-690C-1	-	1, Appli
17	20	95.2		2	US-09-265-690C-4	Sequence	4, Appli
18	20	95.2	5 2	2	US-08-153-847-1	Sequence	1, Appli
19	20	95.2	5 2	2	US-09-635-266-4		4, Appli
20	20	95.2		2	US-10-230-133-4	-	4, Appli
21	20	95.2					
				2	US-09-623-548A-604		604, App
22	20	95.2		2	US-10-695-536-4	Sequence	4, Appli
23	20	95.2	5 2	2	US-10-668-565-1	Sequence	1, Appli
24	20	95.2	5 2	2	US-10-134-187-3		3, Appli
25	20	95.2		2	US-09-657-276-604		604, App
26	20	95.2		5	PCT-US95-05600-78		
						-	78, Appl
27	17	81.0		L	US-07-737-371E-48	_	48, Appl
28	15	71.4		2	US-09-635-266-2	Sequence	2, Appli
29	15	71.4	3 2	2	US-10-230-133-2	Sequence	2, Appli
30	15	71.4	3 2	2	US-09-623-548A-624		624, App
31	15	71.4		2	US-10-695-536-2	_	2, Appli
32	15	71.4		2	US-09-657-276-624		
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33	15	71.4		L	US-08-441-591-63	_	63, Appl
34	15	71.4		L	US-08-303-362A-63		63, Appl
35	15	71.4	4 1	L	US-08-070-301-8	Sequence	8, Appli
3.6	15	71.4	4 2	2	US-09-265-690C-2	Sequence	2, Appli
37	15	71.4	4 2	2	US-09-635-266-3		3, Appli
38	15	71.4	4 2	,	US-10-230-133-3	<del>-</del>	3, Appli
39	15	71.4		2	US-09-623-548A-623		623, App
40	15	71.4		2	US-09-623-548A-971	Sequence	
41	15	71.4	4 2	2	US-09-623-548A-998	Sequence	998, App
42	15	71.4	4 2	2	US-10-695-536-3	Sequence	3, Appli
43	15	71.4	4 2	2	US-09-657-276-623	Sequence	623, App
44	15	71.4	4 2	2	US-09-657-276-971	_	971, App
45	15	71.4		2	US-09-657-276-998	_	998, App
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46	15	71.4		5	PCT-US95-05600-80		80, Appl
47	15	71.4		L	US-08-460-343B-55	Sequence	55, Appl
48	15	71.4	5 1	L	US-08-398-028B-55	Sequence	55, Appl
49	15	71.4	5 1	L	US-08-504-265B-55		55, Appl
50	15	71.4	5 1	1	US-08-070-301-6		6, Appli
51	15	71.4	5 1		US-07-737-371E-47		
							47, Appl
52	15	71.4	5 1		US-07-737-371E-49	Sequence	
53	15	71.4	5 2		US-09-623-548A-565	Sequence	
54	15	71.4	5 2	2	US-09-623-548A-970	Sequence	970, App
55	15	71.4	5 2	2	US-09-623-548A-997		997, App
56	15	71.4	5 2		US-09-657-276-565		565, App
57	15	71.4	5 2		US-09-657-276-970		970, App
	15		5 2				
58		71.4			US-09-657-276-997		997, App
59	14	66.7		L	US-07-690-284A-6	Sequence	
60	14	66.7	5 1		US-07-805-727-28		28, Appl
61	14	66.7	5 1	L	US-08-201-081-5	Sequence	5, Appli

## SCORE Search Results Details for Application 10805881 and Search Result us-10-805-881 4.max.rapbm.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10805881 and Search Result us-10-8( 4.max.rapbm.

start

Go Back to p

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2006, 17:57:39; Search time 119.5 Seconds

(without alignments)

19.381 Million cell updates/sec

Title: US-10-805-881-4

Perfect score: 21

Sequence: 1 FXGLM 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 37972

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:\*

> 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:\* 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:\*

> 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:\* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:\* 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	95.2	<b></b> 5	 3	US-09-265-690C-1	Sequence 1, Appli

•			_	_		_	
2	20	95.2	5	3	US-09-265-690C-4	Sequence	
3	20	95.2	5	4	US-10-230-133-4	Sequence	
4	20	95.2	5	4	US-10-053-669-1	Sequence	l, Appli
5	20	95.2	5	4	US-10-053-669-4	Sequence	4, Appli
6	20	95.2	5	4	US-10-134-187-3	Sequence	3, Appli
7	20	95.2	5	4	US-10-688-741-3	Sequence	3, Appli
8	20	95.2	5	4	US-10-695-536-4	Sequence	4, Appli
9	20	95.2	5	4	US-10-805-881-1	Sequence	
10	20	95.2	5	4	US-10-805-881-4	Sequence	
11	20	95.2	5	5	US-10-720-039-3	Sequence	
12	20	95.2	5	5	US-10-497-628-15	Sequence	
13	20	95.2	5	5	US-10-451-304-12	Sequence	
14	20	95.2	5	6	US-11-018-690-4	Sequence	
15	20	95.2	5	6	US-11-066-697-604	Sequence	
16	20	95.2	5	6	US-11-025-494-3		
17	20	95.2	5	6		Sequence	
					US-11-041-270A-12	Sequence	
18	20	95.2	5	6	US-11-292-460-4	Sequence	
19	17	81.0	5	4	US-10-168-789A-32	Sequence	
20	17	81.0	5	4	US-10-168-789A-39	Sequence	
21	17	81.0	5	5	US-10-497-628-16	Sequence	
22	15	71.4	3	4	US-10-230-133-2	Sequence	2, Appli
23	15	71.4	3	4	US-10-695-536-2	Sequence :	2, Appli
24	15	71.4	3	6	US-11-018-690-2	Sequence	2, Appli
25	15	71.4	3	6	US-11-066-697-624	Sequence	
26	15	71.4	3	6	US-11-041-270A-14	Sequence	
27	15	71.4	3	6	US-11-292-460-2	Sequence	
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30	15	71.4	4	4	US-10-053-669-2	Sequence :	
31	15	71.4	4	4	US-10-695-536-3		
32	15	71.4	4	4	US-10-805-881-2	Sequence	
		_				Sequence	
33	15	71.4	4	5	US-10-497-628-2	Sequence :	
34	15	71.4	4	5	US-10-821-240A-244	Sequence	
35	15	71.4	4	5	US-10-821-240A-270	Sequence :	
36	15	71.4	4	6	US-11-018-690-3	Sequence	
37	15	71.4	4	6	US-11-066-697-623	Sequence	
38	15	71.4	4	6	US-11-066-697-971	Sequence	971, App
39	15	71.4	4	6	US-11-066-697-998	Sequence	998, App
40	15	71.4	4	6	US-11-041-270A-13	Sequence	13, Appl
41	15	71.4	4	6	US-11-292-460-3	Sequence	3, Appli
42	15	71.4	5	4	US-10-128-520-360	Sequence	360, App
43	15	71.4	5	4	US-10-346-737A-30	Sequence	30, Appl
44	15	71.4	5	5	US-10-497-628-17	Sequence	
45	15	71.4	5	6	US-11-066-697-565	Sequence	
46	15	71.4	5	6	US-11-066-697-970	Sequence	
47	15	71.4	5	6	US-11-066-697-997	Sequence	
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50	14	66.7	5	4	US-10-190-951-28	Sequence	
51	14	66.7	5	4	US-10-454-566-10	Sequence	
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53	14	66.7 66.7	5	4 4	US-10-454-566-17 US-10-436-549-565	Sequence	
						Sequence	
54	14	66.7	5	4	US-10-712-425-565	Sequence	
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58	14	66.7	5	5	US-10-996-573-10	Sequence	
59	14	66.7	5	5	US-10-996-573-17	Sequence	17, Appl
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61	14	66.7	5	6	US-11-066-697-884	Sequence	
62	14	66.7	5	6	US-11-066-697-885	Sequence	